identified as the aimed N-biotinylcysteic acid using MALDI-TOF MS.

(2) Coupling of N-biotinylcysteic acid to peptide

As a model peptide, laminin pentapeptide (PEPTIDE INSTITUTE, Inc.) was used. The amino acid sequence of the laminin pentapeptide is as follows: Tyr-Ile-Gly-Ser-Arg-NH_2 (SEQ ID NO: 1). In this sequence, the arginine residue is amidated and is represented as Arg-NH_2. 2μl of 1mM dimethyl formamide solution of N-biotinylcysteic acid, 0.6μl of dimethylformamide solution containing 0.5M HBTU (2-[1H-benzo triazole-1-yl]-1,1,3,3- tetramethyluronium hexafluoro phosphate) and 0.5M HOBt (N-hydroxybenzotriazole), and 0.6μl of 1M dimethylformamide solution of diisopropylethylamine were mixed with one another. The mixture was then added to 2μl of 2mM dimethylformamide solution of laminin pentapeptide, and the reaction was allowed to proceed at room temperature for 30min. After the reaction was completed, the reaction mixture was diluted with 0.1w% aqueous solution of trifluoroacetic acid and was subjected to PSD analysis by MALDI-TOF MS.

Fig. 1 shows the PSD spectra of laminin pentapeptide that is coupled to N-ciotinylcysteic acid. Fig. 2 shows the PSD spectra of laminin pentapeptide that is not coupled to N-biotinylcysteic acid. In each figure, horizontal axis indicates the mass-to-charge ratio of the ions (m/z), whereas vertical axis indicates the relative intensity of the ions